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APPLICATION NO.	FILING DATE	FIRST NAMED INVENTOR	ATTORNEY DOCKET NO.	CONFIRMATION NO.
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EXAMINER	
TRAN, MY CHAU T	
ART UNIT	**PAPER NUMBER**
1639	

DATE MAILED: 06/09/2005

Please find below and/or attached an Office communication concerning this application or proceeding.

Office Action Summary	Application No.	Applicant(s)	
	09/748,793	AEBERSOLD ET AL.	
	Examiner	Art Unit	
	MY-CHAU T. TRAN	1639	

-- The MAILING DATE of this communication appears on the cover sheet with the correspondence address --

Period for Reply

A SHORTENED STATUTORY PERIOD FOR REPLY IS SET TO EXPIRE 3 MONTH(S) FROM THE MAILING DATE OF THIS COMMUNICATION.

- Extensions of time may be available under the provisions of 37 CFR 1.136(a). In no event, however, may a reply be timely filed after SIX (6) MONTHS from the mailing date of this communication.
- If the period for reply specified above is less than thirty (30) days, a reply within the statutory minimum of thirty (30) days will be considered timely.
- If NO period for reply is specified above, the maximum statutory period will apply and will expire SIX (6) MONTHS from the mailing date of this communication.
- Failure to reply within the set or extended period for reply will, by statute, cause the application to become ABANDONED (35 U.S.C. § 133). Any reply received by the Office later than three months after the mailing date of this communication, even if timely filed, may reduce any earned patent term adjustment. See 37 CFR 1.704(b).

Status

1)☒ Responsive to communication(s) filed on *06 April 2005*.

2a)☒ This action is **FINAL**. 2b)☐ This action is non-final.

3)☐ Since this application is in condition for allowance except for formal matters, prosecution as to the merits is closed in accordance with the practice under *Ex parte Quayle*, 1935 C.D. 11, 453 O.G. 213.

Disposition of Claims

4)☒ Claim(s) *1-52* is/are pending in the application.

4a) Of the above claim(s) *24-43* is/are withdrawn from consideration.

5)☐ Claim(s) _____ is/are allowed.

6)☒ Claim(s) *1-23 and 44-52* is/are rejected.

7)☐ Claim(s) _____ is/are objected to.

8)☐ Claim(s) _____ are subject to restriction and/or election requirement.

Application Papers

9)☐ The specification is objected to by the Examiner.

10)☒ The drawing(s) filed on *26 December 2000* is/are: a)☒ accepted or b)☐ objected to by the Examiner.

Applicant may not request that any objection to the drawing(s) be held in abeyance. See 37 CFR 1.85(a).

Replacement drawing sheet(s) including the correction is required if the drawing(s) is objected to. See 37 CFR 1.121(d).

11)☐ The oath or declaration is objected to by the Examiner. Note the attached Office Action or form PTO-152.

Priority under 35 U.S.C. § 119

12)☐ Acknowledgment is made of a claim for foreign priority under 35 U.S.C. § 119(a)-(d) or (f).

a)☐ All b)☐ Some * c)☐ None of:

1.☐ Certified copies of the priority documents have been received.

2.☐ Certified copies of the priority documents have been received in Application No. _____.

3.☐ Copies of the certified copies of the priority documents have been received in this National Stage application from the International Bureau (PCT Rule 17.2(a)).

* See the attached detailed Office action for a list of the certified copies not received.

Attachment(s)

1) ☒ Notice of References Cited (PTO-892)
2) ☐ Notice of Draftsperson's Patent Drawing Review (PTO-948)
3) ☒ Information Disclosure Statement(s) (PTO-1449 or PTO/SB/08) Paper No(s)/Mail Date *5/16/05*.
4) ☐ Interview Summary (PTO-413) Paper No(s)/Mail Date. _____ .
5) ☐ Notice of Informal Patent Application (PTO-152)
6) ☐ Other: _____.

HC

DETAILED ACTION

1. A request for continued examination under 37 CFR 1.114, including the fee set forth in 37 CFR 1.17(e), was filed in this application after final rejection. Since this application is eligible for continued examination under 37 CFR 1.114, and the fee set forth in 37 CFR 1.17(e) has been timely paid, the finality of the previous Office action has been withdrawn pursuant to 37 CFR 1.114. Applicant's submission filed on 04/06/2005 has been entered.

Application and Claims Status

2. Applicant's response filed 04/06/2005 is acknowledged and entered.

3. Claims 1, and 13 were amended by the amendment filed on 06/21/2004.

4. Claims 1, and 13 were amended, and claims 51-52 were added by the amendment filed on 08/07/2003.

5. Claims 1-52 are pending.

Election/Restrictions

6. Claims 24-43 are withdrawn from further consideration pursuant to 37 CFR 1.142(b), as being drawn to ***nonelected inventions***, there being no allowable generic or linking claim. Applicant timely traversed the restriction (election) requirement in the reply filed on 07/26/2002.

7. This application contains claims 24-43 that are drawn to inventions nonelected with traverse the reply filed on 07/26/200. A complete reply to the final rejection must include cancellation of nonelected claims or other appropriate action (37 CFR 1.144) See MPEP § 821.01.

8. Claims 1-23, and 44-52 are treated on the merit in this Office Action.

Information Disclosure Statement

9. The information disclosure statement (IDS) filed on 05/16/2005 has been reviewed, and its references have been considered as noted on PTO-1449 form(s).

Maintained Rejection(s)

10. The text of those sections of Title 35, U.S. Code not included in this action can be found in a prior Office action.

11. Claims 1, and 4-8 are rejected under 35 U.S.C. 102(a) as being anticipated by Masselon et al. (*Anal. Chem.*, **2000**, 72:1918-1924) for the reasons of record set forth in the previous Office Action.

12. Claims 1-2, 8-12, and 50 are rejected under 35 U.S.C. 102(b) as being anticipated by Yates, III (*J. Mass Spectrom.*, **1998**, 33(1):1-19) for the reasons of record set forth in the previous Office Action.

13. Claims 1-2, 12, 44, and 50 are rejected under 35 U.S.C. 102(b) as being anticipated by Clauser et al. (*Proc. Natl. Acad. Sci.*, **1995**, 92:5072-5076) for the reasons of record set forth in the previous Office Action.

14. Claims 1-12, and 44-50 are rejected under 35 U.S.C. 103(a) as being unpatentable over Clauser et al. (*Proc. Natl. Acad. Sci.*, **1995**, 92:5072-5076) and Gygi et al. (*Nat. Biotechnol.*; 17(10):994-999; 1999) for the reasons of record set forth in the previous Office Action.

15. Claims 13-23 and 51-52 are rejected under 35 U.S.C. 103(a) as being unpatentable over Clauser et al. (*Proc. Natl. Acad. Sci.*, **1995**, 92:5072-5076) and Gygi et al. (*Nat. Biotechnol.*; 17(10):994-999; 1999) for the reasons of record set forth in the previous Office Action.

Response to Arguments

16. Claims 1, and 4-8 are rejected under 35 U.S.C. 102(a) as being anticipated by Masselon et al. (*Anal. Chem.*, **2000**, 72:1918-1924) for the reasons of record set forth in the previous Office Action.

Masselon et al. disclose the method of identifying the polypeptides in a sample mixture by mass spectrometric approach wherein the mass data of the sample is compared with the mass data of a database in order to identify the polypeptides in a sample mixture (pg. 1922, fig. 3; pg. 1921, left col., lines 25-29; pg. 1921, right col., lines 13-26). The method comprises of obtaining the mass of the peptide fragment by mass spectrometry of the sample (refers to step (a) of claim 1) and then the search for the identification of the polypeptides. The search is performed by first generating a list of the masses of all possible tryptic fragments protein (empirically determined characteristic/second characteristic) and compared to a list of masses of the parent ions to create a database (annotated polypeptide index) to use for the identification of the polypeptides in a sample (refers to step (b) and (c) of claim 1). The fragment mass is determined by the accuracy of the 1 ppm or greater (pg. 1919, right col., lines 28-33) (refers to claims 4-8). Therefore, the method of Masselon et al. anticipates the presently claimed method.

17. Applicant's arguments directed to the rejection under 35 USC 102(a) as being anticipated by Masselon et al. (*Anal. Chem.*, **2000**, 72:1918-1924) for claims 1, and 4-8 were considered but they are not persuasive for the following reasons.

Applicant contends that the method of Masselon et al. does not anticipate the presently claimed method because Masselon et al. does not teach the use of a database of empirically determined characteristics and therefore provides no teaching of the generation of an annotated polypeptide index having at least one empirically determined characteristic and applicant supports this assertion by providing an expert opinion by Dr. David G. Camp II in the declaration under 37 CFR 1.132. Thus the method of Masselon et al. does not anticipate the presently claimed method.

Applicant's arguments are not convincing since the method of Masselon et al. does anticipate the presently claimed method.

First, the method of Masselon et al. does teach using a database of empirically determined characteristics and therefore does teach the generation of an annotated polypeptide index having at least one empirically determine characteristic (see e.g. pg. 1922, fig. 3; pg. 1921, left col., lines 25-29; pg. 1921, right col., lines 13-26). Additionally, Masselson et al. disclose that "*The database used consisted of predicted proteins initially reported for the full Caenorhabditis elegans genome sequence*[18] *and contained 19 106 putative proteins, corresponding to 918 655 possible tryptic fragments (excluding partial digestion products)*", i.e. the database contains known genomic sequence of *Caenorhabditis elegans*, and the tryptic fragments of this sequence. Thus the database contains "empirical" data, which Masselon et al. supported by the cited reference #18, i.e. *The C. elegans consortium (Science, 1998, 282, 2012-2018)*. Applicant has not shown that these "predicted" proteins are not "empirical" proteins. Moreover, applicant's arguments do not rise to the level of factual evidence. See MPEP §

716.01(c): The arguments of counsel cannot take the place of evidence in the record. *In re Schulze*, 346 F.2d 600, 602, 145 USPQ 716, 718 (CCPA 1965).

Second, the expert opinion by Dr. David G. Camp II in the declaration under 37 CFR 1.132 is inadequate to overcome this rejection because there is no factual evidence supporting the statement (as discussed in the Office Action mailed on 9/28/2004), i.e. "*The expert opinion by Dr. David G. Camp II in the declaration under 37 CFR 1.132 is inadequate to overcome the rejections of claims 1-23, and 44-52 based upon the cited prior art of Masselon et al. (Anal. Chem., **2000**, 72:1918-1924), Clauser et al. (Proc. Natl. Acad. Sci., **1995**, 92:5072-5076), and Gygi et al. (Nat. Biotechnol.; 17(10):994-999; 1999) because there is no factual evidence supporting the statement. That is the expert opinion by Dr. David G. Camp II fails to set forth facts that the database (refers to the claimed annotated polypeptide index) of the cited prior art does not include an empirically determine characteristic for each polypeptides as claimed in the instant method such as a side-by-side comparison of the prior art database and the instant claimed database use in the claimed method for identifying a polypeptide. (See MPEP § 716.01(c)).*"

Therefore, the method of Masselon et al. does anticipate the presently claimed method, and this rejection is maintained.

18. Claims 1-2, 8-12, and 50 are rejected under 35 U.S.C. 102(b) as being anticipated by Yates, III (*J. Mass Spectrom.*, **1998**, 33(1):1-19) for the reasons of record set forth in the previous Office Action.

Yates, III disclosed two different types of methods identifying polypeptides by mass spectrometry one is mass mapping (pg. 8, right col., lines 10-13 to pg. 9, left col., lines 1-5) and the second is by 'shotgun' identification of proteins in mixtures (pg. 13, right col., lines 16-33 to pg. 14, left col., lines 1-5; fig. 8). In mass mapping the determined mass is compared with database

information of one organism to identify the similar or homologous protein of another organism to identify the polypeptide (pg. 8, right col., lines 10-13 to pg. 9, left col., lines 1-5). In the 'shotgun' identification of proteins in mixtures, the proteins in the mixture is digested and then the protein fragment of the digested mixture is analyzed by mass spectrometry (pg. 13, right col., lines 16-21). The data is compared using computer algorithms and databases in order to reconstruct the identities of the proteins (pg. 13, right col., lines 31-33 to pg. 14, left col., lines 1-5). Therefore, the methods of Yates, III anticipate the presently claimed method.

19. Applicant's arguments directed to the rejection under 35 USC 102(b) as being anticipated by Yates, III (*J. Mass Spectrom.*, **1998**, 33(1):1-19) for claims 1-2, 8-12, and 50 were considered but they are not persuasive for the following reasons.

Applicant argues that the method of Yates, III does not anticipate the presently claimed method because Yates does not teach the use of a database of empirically determined characteristics and therefore provides no teaching of the generation of an annotated polypeptide index having at least one empirically determined characteristic and applicant supports this assertion by providing an expert opinion by Dr. David G. Camp II in the declaration under 37 CFR 1.132. Thus the method of Yates, III does not anticipate the presently claimed method.

Applicant's arguments are not convincing since the method of Yates, III does anticipate the presently claimed method.

First, the expert opinion by Dr. David G. Camp II in the declaration under 37 CFR 1.132 is insufficient to overcome this rejection because a declaration under 37 CFR 1.132 is insufficient to overcome the statutory bar (as discussed in the Office Action mailed on 9/28/2004), i.e. "*The declaration under 37 CFR 1.132 is insufficient to overcome the statutory bar, i.e. the rejections under 35 U.S.C. 102(b), with regard to the cited prior art of Yates, III (J. Mass Spectrom., **1998**, 33(1):1-19), and Clauser et al. (Proc. Natl. Acad. Sci., **1995**, 92:5072-5076). (See MPEP § 706.02(b))*".

Second, Yates, III does teach using a database of empirically determined characteristics and therefore does teach the generation of an annotated polypeptide index having at least one

empirically determine characteristic (see e.g. pg. 8, right col., lines 10-13 to pg. 9, left col., lines 1-5; pg. 13, right col., lines 16-33 to pg. 14, left col., lines 1-5; fig. 8). Additionally, the databases disclose by Yates is sequence databases, i.e. the database contain known protein sequences (see e.g. figs. 3 and 4; pg. 14, left col., line 28 thru pg. 14, right col., line 3). Thus these databases contain "empirical" data. Applicant has not shown that these sequence databases does not "empirical" protein sequences. Moreover, applicant's arguments do not rise to the level of factual evidence. See MPEP § 716.01(c): The arguments of counsel cannot take the place of evidence in the record. *In re Schulze*, 346 F.2d 600, 602, 145 USPQ 716, 718 (CCPA 1965).

Therefore, the method of Yates, III does anticipate the presently claimed method, and this rejection is maintained

20. Claims 1-2, 12, 44, and 50 are rejected under 35 U.S.C. 102(b) as being anticipated by Clauser et al. (*Proc. Natl. Acad. Sci.*, **1995**, 92:5072-5076) for the reasons of record set forth in the previous Office Action.

Clauser et al. disclosed a method of identifying and characterizing protein by mass spectrometry (pg. 5073, left col., lines 41-63; fig. 2). The method step comprise excised protein spot from several gels, pooling spots of identical mass pI (second characteristic), and peptide separation by HPLC (chromatography) (pg. 5073, left col., lines 46-49; fig. 2) (refers to claim 12, 44, and 50); determining the mass of each of these peptides by mass spectrometry (first characteristic) (pg. 5073, left col., lines 54-55; fig. 2); and search peptide mass database (annotated polypeptide index) with the experimentally determine "characteristics" to identify the protein (pg. 5073, left col., lines 60-63; fig. 2). The peptide database is MOWSE, which is a non-sequence database (pg. 5073; left col., lines 34-37). Therefore, the method of Clauser et al. anticipate the presently claimed method.

21. Applicant's arguments directed to the rejection under 35 USC 102(b) as being anticipated by Clauser et al. (*Proc. Natl. Acad. Sci.*, **1995**, 92:5072-5076) for claims 1-2, 12, 44, and 50 were considered but they are not persuasive for the following reasons.

Applicant alleges that the method of Clauser et al. does not anticipate the presently claimed method because Clauser et al. does not teach the use of a database of empirically

determined characteristics and therefore provides no teaching of the generation of an annotated polypeptide index having at least one empirically determined characteristic and applicant supports this assertion by providing an expert opinion by Dr. David G. Camp II in the declaration under 37 CFR 1.132. Thus the method of Clauser et al. does not anticipate the presently claimed method.

Applicant's arguments are not convincing since the method of Clauser et al. does anticipate the presently claimed method.

First, the expert opinion by Dr. David G. Camp II in the declaration under 37 CFR 1.132 is insufficient to overcome this rejection because a declaration under 37 CFR 1.132 is insufficient to overcome the statutory bar (as discussed in the Office Action mailed on 9/28/2004), i.e. "*The declaration under 37 CFR 1.132 is insufficient to overcome the statutory bar, i.e. the rejections under 35 U.S.C. 102(b), with regard to the cited prior art of Yates, III (J. Mass Spectrom., **1998**, 33(1):1-19), and Clauser et al. (Proc. Natl. Acad. Sci., **1995**, 92:5072-5076). (See MPEP § 706.02(b))*".

Second, Clauser et al. does teach using a database of empirically determined characteristics and therefore does teach the generation of an annotated polypeptide index having at least one empirically determine characteristic (see e.g. pg. 5073, left col., lines 60-63; fig. 2). Additionally, the databases of OWL and MOWSE comprise known protein sequences (see enclose information regarding these databases). Thus these databases contain "empirical" data. Applicant has not shown that these sequence databases does not "empirical" protein sequences. Moreover, applicant's arguments do not rise to the level of factual evidence. See MPEP §

716.01(c): The arguments of counsel cannot take the place of evidence in the record. *In re Schulze*, 346 F.2d 600, 602, 145 USPQ 716, 718 (CCPA 1965).

Therefore, the method of Clauser et al. does anticipate the presently claimed method, and this rejection is maintained.

22. Claims 1-12, and 44-50 are rejected under 35 U.S.C. 103(a) as being unpatentable over Clauser et al. (*Proc. Natl. Acad. Sci.*, **1995**, 92:5072-5076) and Gygi et al. (*Nat. Biotechnol.*; 17(10):994-999; 1999) for the reasons of record set forth in the previous Office Action.

Clauser et al. disclosed a method of identifying and characterizing protein by mass spectrometry (pg. 5073, left col., lines 41-63; fig. 2). The method step comprise excised protein spot from several gels pooling spots of identical mass pI (second characteristic), and peptide separation by HPLC (chromatography) (pg. 5073, left col., lines 46-49; fig. 2) (refers to claim 12, 44, and 50); determining the mass of each of these peptides by mass spectrometry (first characteristic) (pg. 5073, left col., lines 54-55; fig. 2); and search peptide mass database (annotated polypeptide index) with the experimentally determine "characteristics" to identify the protein (pg. 5073, left col., lines 60-63; fig. 2). The peptide database is MOWSE, which is a non-sequence database (pg. 5073; left col., lines 34-37).

Additionally, the limitation of the number of characteristics of the polypeptide (e.g. claims 2, and 9-11), the type of chromatography (e.g. claims 45-49, and the limitation of the degree of mass accuracy (e.g. claims 4-8) would be considered a choice as experimental design and is considered within the purview of the prior art.

The method of Clauser et al. does not expressly disclose method step of quantitating the amount of polypeptide in a sample.

Gygi et al. disclose a method of quantitative analysis of protein using isotope-coded affinity tags (Abstract; pg. 994, right col., lines 6-9; pg. 996, left col., line 10 to right col., line 10; fig. 2 and 3).

It would have been obvious to a person of ordinary skill in the art at the time the invention was made to include the method step of quantitating the amount of polypeptide in a sample as taught by Gygi et al. in the method of Clauser et al. One of ordinary skill in the art would have been motivated to include the method step of quantitating the amount of polypeptide in a sample in the method of Clauser et al. for the advantage of the relative quantities as well as the identity of the polypeptide in a single automated operation (Gygi: pg 995, right column, line 1-2) since both Clauser et al. and Gygi et al. disclose the method of detecting polypeptide by mass spectrometry (Clauser: pg. 5073, left col., lines 54-55; Gygi: pg. 995, left col., line 7 to right col., line 2). One of ordinary skill in the art would have reasonably expectation of success in the combination of Clauser et al. and Gygi et al. because Gygi et al. disclose examples in the application of the method to quantitative analysis of protein in different sample type such as standard mixture and proteome analysis (pg. 996-998).

23. Applicant's arguments directed to the rejection under 35 USC 103(a) as being unpatentable over Clauser et al. (*Proc. Natl. Acad. Sci.*, **1995**, 92:5072-5076) and Gygi et al. (*Nat. Biotechnol.*; 17(10):994-999; 1999) for claims 1-12, and 44-50were considered but they are not persuasive for the following reasons.

Applicant alleges that the method combination of Clauser et al. and Gygi et al. is not obvious over the presently claimed method because Clauser et al. does not teach or suggest the presently claimed method and Gygi et al. does not cure the deficiencies. Additionally, applicant supports this assertion by providing an expert opinion by Dr. David G. Camp II in the declaration under 37 CFR 1.132.

Applicant's arguments are not convincing since the method combination of Clauser et al. and Gygi et al. is obvious over the presently claimed method.

First, the expert opinion by Dr. David G. Camp II in the declaration under 37 CFR 1.132 is inadequate to overcome this rejection because there is no factual evidence supporting the statement (as discussed in the Office Action mailed on 9/28/2004), i.e. "*The expert opinion by Dr. David G. Camp II in the declaration under 37 CFR 1.132 is inadequate to overcome the rejections of claims 1-23, and 44-52 based upon the cited prior art of Masselon et al. (Anal. Chem., **2000**, 72:1918-1924), Clauser et al. (Proc. Natl. Acad. Sci., **1995**, 92:5072-5076), and Gygi et al. (Nat. Biotechnol.; 17(10):994-999; 1999) because there is no factual evidence supporting the statement. That is the expert opinion by Dr. David G. Camp II fails to set forth facts that the database (refers to the claimed annotated polypeptide index) of the cited prior art does not include an empirically determine characteristic for each polypeptides as claimed in the instant method such as a side-by-side comparison of the prior art database and the instant claimed database use in the claimed method for identifying a polypeptide. (See MPEP § 716.01(c)).*"

Second, Clauser et al. does not teach or suggest the presently claimed method. Clauser et al. does teach using a database of empirically determined characteristics and therefore does teach

the generation of an annotated polypeptide index having at least one empirically determine characteristic (see e.g. pg. 5073, left col., lines 60-63; fig. 2). Additionally, the databases of OWL and MOWSE comprise known protein sequences (see enclose information regarding these databases). Thus these databases contain "empirical" data. Applicant has not shown that these sequence databases does not "empirical" protein sequences. Moreover, applicant's arguments do not rise to the level of factual evidence. See MPEP § 716.01(c): The arguments of counsel cannot take the place of evidence in the record. *In re Schulze*, 346 F.2d 600, 602, 145 USPQ 716, 718 (CCPA 1965).

Therefore, the method combination of Clauser et al. and Gygi et al. is obvious over the presently claimed method, and this rejection is maintained.

24. Claims 13-23 and 51-52 are rejected under 35 U.S.C. 103(a) as being unpatentable over Clauser et al. (*Proc. Natl. Acad. Sci.*, **1995**, 92:5072-5076) and Gygi et al. (*Nat. Biotechnol.*; 17(10):994-999; 1999) for the reasons of record set forth in the previous Office Action.

Clauser et al. disclosed a method of identifying and characterizing protein by mass spectrometry (pg. 5073, left col., lines 41-63; fig. 2). The method step comprise excised protein spot from several gels pooling spots of identical mass pI (second characteristic), and peptide separation by HPLC (chromatography) (pg. 5073, left col., lines 46-49; fig. 2) (refers to claim 12, 44, and 50); determining the mass of each of these peptides by mass spectrometry (first characteristic) (pg. 5073, left col., lines 54-55; fig. 2); and search peptide mass database (annotated polypeptide index) with the experimentally determine "characteristics" to identify the protein (pg. 5073, left col., lines 60-63; fig. 2). The peptide database is MOWSE, which is a non-sequence database (pg. 5073; left col., lines 34-37).

Additionally, the limitation of the number of characteristics of the polypeptide (e.g. claims 2, and 9-11), the type of chromatography (e.g. claims 45-49, and the limitation of the degree of mass accuracy (e.g. claims 4-8) would be considered a choice as experimental design and is considered within the purview of the prior art.

The method of Clauser et al. does not expressly disclose method step of quantitating the amount of polypeptide in a sample.

Gygi et al. disclose a method of quantitative analysis of protein using isotope-coded affinity tags (Abstract; pg. 994, right col., lines 6-9; pg. 996, left col., line 10 to right col., line 10; fig. 2 and 3).

It would have been obvious to a person of ordinary skill in the art at the time the invention was made to include the method step of quantitating the amount of polypeptide in a sample as taught by Gygi et al. in the method of Clauser et al. One of ordinary skill in the art would have been motivated to include the method step of quantitating the amount of polypeptide in a sample in the method of Clauser et al. for the advantage of the relative quantities as well as the identity of the polypeptide in a single automated operation (Gygi: pg 995, right column, line 1-2) since both Clauser et al. and Gygi et al. disclose the method of detecting polypeptide by mass spectrometry (Clauser: pg. 5073, left col., lines 54-55; Gygi: pg. 995, left col., line 7 to right col., line 2). One of ordinary skill in the art would have reasonably expectation of success in the combination of Clauser et al.

and Gygi et al. because Gygi et al. disclose examples in the application of the method to quantitative analysis of protein in different sample type such as standard mixture and proteome analysis (pg. 996-998).

25. Applicant's arguments directed to the rejection under 35 USC 103(a) as being unpatentable over Clauser et al. (*Proc. Natl. Acad. Sci.*, **1995**, 92:5072-5076) and Gygi et al. (*Nat. Biotechnol.*; 17(10):994-999; 1999) for claims 13-23 and 51-52 were considered but they are not persuasive for the following reasons.

Applicant contends that the method combination of Clauser et al. and Gygi et al. is not obvious over the presently claimed method because Clauser et al. does not teach or suggest the presently claimed method and Gygi et al. does not cure the deficiencies. Additionally, applicant supports this assertion by providing an expert opinion by Dr. David G. Camp II in the declaration under 37 CFR 1.132.

Applicant's arguments are not convincing since the method combination of Clauser et al. and Gygi et al. is obvious over the presently claimed method.

First, the expert opinion by Dr. David G. Camp II in the declaration under 37 CFR 1.132 is inadequate to overcome this rejection because there is no factual evidence supporting the statement (as discussed in the Office Action mailed on 9/28/2004), i.e. "*The expert opinion by Dr. David G. Camp II in the declaration under 37 CFR 1.132 is inadequate to overcome the rejections of claims 1-23, and 44-52 based upon the cited prior art of Masselon et al. (Anal. Chem., **2000**, 72:1918-1924), Clauser et al. (Proc. Natl. Acad. Sci., **1995**, 92:5072-5076), and Gygi et al. (Nat. Biotechnol.; 17(10):994-999; 1999) because there is no factual evidence supporting the statement. That is the expert opinion by Dr. David G. Camp II fails to set forth facts that the database (refers to the claimed annotated polypeptide index) of the cited prior art does not include an empirically determine characteristic for each polypeptides as claimed in the*

instant method such as a side-by-side comparison of the prior art database and the instant claimed database use in the claimed method for identifying a polypeptide. (See MPEP § 716.01(c))."

Second, Clauser et al. does not teach or suggest the presently claimed method. Clauser et al. does teach using a database of empirically determined characteristics and therefore does teach the generation of an annotated polypeptide index having at least one empirically determine characteristic (see e.g. pg. 5073, left col., lines 60-63; fig. 2). Additionally, the databases of OWL and MOWSE comprise known protein sequences (see enclose information regarding these databases). Thus these databases contain "empirical" data. Applicant has not shown that these sequence databases does not "empirical" protein sequences. Moreover, applicant's arguments do not rise to the level of factual evidence. See MPEP § 716.01(c): The arguments of counsel cannot take the place of evidence in the record. *In re Schulze*, 346 F.2d 600, 602, 145 USPQ 716, 718 (CCPA 1965).

Therefore, the method combination of Clauser et al. and Gygi et al. is obvious over the presently claimed method, and this rejection is maintained.

Conclusion

26. All claims are drawn to the same invention claimed in the application prior to the entry of the submission under 37 CFR 1.114 and could have been finally rejected on the grounds and art of record in the next Office action if they had been entered in the application prior to entry under 37 CFR 1.114. Accordingly, **THIS ACTION IS MADE FINAL** even though it is a first action after the filing of a request for continued examination and the submission under 37 CFR 1.114.

See MPEP § 706.07(b). Applicant is reminded of the extension of time policy as set forth in 37 CFR 1.136(a).

A shortened statutory period for reply to this final action is set to expire THREE MONTHS from the mailing date of this action. In the event a first reply is filed within TWO MONTHS of the mailing date of this final action and the advisory action is not mailed until after the end of the THREE-MONTH shortened statutory period, then the shortened statutory period will expire on the date the advisory action is mailed, and any extension fee pursuant to 37 CFR 1.136(a) will be calculated from the mailing date of the advisory action. In no event, however, will the statutory period for reply expire later than SIX MONTHS from the mailing date of this final action.

Any inquiry concerning this communication or earlier communications from the examiner should be directed to My-Chau T. Tran whose telephone number is 571-272-0810. The examiner can normally be reached on Monday: 8:00-2:30; Tuesday-Thursday: 7:30-5:00; Friday: 8:00-3:30.

If attempts to reach the examiner by telephone are unsuccessful, the examiner's supervisor, Andrew J. Wang can be reached on 571-272-0811. The fax phone number for the organization where this application or proceeding is assigned is 571-273-8300.

Information regarding the status of an application may be obtained from the Patent Application Information Retrieval (PAIR) system. Status information for published applications may be obtained from either Private PAIR or Public PAIR. Status information for unpublished applications is available through Private PAIR only. For more information about the PAIR system, see http://pair-direct.uspto.gov. Should you have questions on access to the Private PAIR system, contact the Electronic Business Center (EBC) at 866-217-9197 (toll-free).

mct
June 6, 2005

PADMASHRI PONNALURI
PRIMARY EXAMINER